REMARKS

The claims of group I, claims 1-15, 27-29, 31 and 34 were elected. The Examiner has withdrawn the restriction to claims 30 and 32-33 and withdrawn from review claims 2, 5 and 8. With this amendment the applicant withdraws claims, 28-30 and 33, which relate to the promoter of the invention and therefore are not within the elected group. Claims 1, 6 and 7 are cancelled. Thus pending in the application are claims 3, 4, 9-15, 27,31, 32 and 34.

Applicant re-submits with this amendment PTO-1449 for the instant application as requested.

The Applicant has also amended the specification to insert sequence identifiers in the Brief Description of Figure 6.

A new abstract and title is submitted with the amendment, as requested.

The objections to the claims have been addressed by amendments to add commas, colons and other changes as proposed by the Examiner.

Section 112 Rejection

The Examiner has rejected claims 1, 3-4, 6-7, 9-15 and 27-33 under section 112, as not complying with the written description requirement, the Examiner saying that the specification only describes a coding sequence from maize that comprises SEQ ID NO:7 while the claims are to sequences that hybridize to SEQ ID NO: 7 or encode SEQ ID NO: 8 and mediate male fertility. The applicant first points out that the reference to SEQ ID NO: 8 appears to be in error, as there is no SEQ ID NO: 8 in the claims or sequence listing. Claim 3 is to a DNA molecule that mediates fertility in plants comprising any one of SEQ ID NOs: 1, 3 or 7 and those that hybridize to the sequences under highly stringent conditions. Claim 13 is to a method of impacting fertility in a plant by impacting a nucleotide sequence encoding SEQ ID NOs: 2 or 4, , the sequence of SEQ ID NOs: 1, 3 or 7 and those which hybridize to any of said sequences under highly stringent conditions. Claim 27 is the expression vector comprising the DNA sequence of claim 3 (previously reciting claim 1). Claim 31 is to plant cells comprising the vector of claim 27. Claim 32 is a method of mediating male fertility in a plant using the vector of claim 27.

Thus all the claims contain both a recitation of structure, that is, sequences encoding SEQ ID NO: 1, 3 or 7 (in the present review, SEQ ID NO: 7) or those encoding the protein of SEQ ID NO: 2 or 4. The Examiner states that description of the function of the nucleic acid is not specific, therefore not descriptive. However, the claims recite structure, and the recitation that the sequences are those which mediate male fertility further adds to the properties such sequences need exhibit.

The applicant also respectfully traverses the rejection to the recitation that it encompasses sequences which hybridize under highly stringent conditions. The sequences are set forth, their source from more than one species is demonstrated, and the conditions of stringent hybridization are set forth in the specification. Thus structure is known and provided. The interim written description guidelines suggest a similar result indicating in Example 9 that in showing the structure of a particular sequence that encodes a particular protein, there is adequate description to support a claim to that sequence and those that hybridize to it under highly stringent conditions. (See http://www.uspto.gov/web/menu/written.pdf). The comments analyze that "a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claims because the highly stringent hybridization conditions set forth in the claim yield structurally similar DNAs. Thus, a representative number of species is disclosed, since highly stringent hybridization conditions in combination with the coding function of DNA and the level of skill and knowledge in the are adequate to determine that applicant was in possession of the claimed invention." Here, too, a person of skill in the art would not expect substantial variation among species included within the claims and the highly stringent hybridization conditions will yield structurally similar DNAs. Further, those sequences are recited in the claims to mediate (amended here to recite "impact") male fertility in a plant. Both property and structure are provided.

Claim 34 is rejected under section 112 as not enabled, the claim reciting a nucleotide sequence as represented in ATCC deposit no. 98931. The Examiner says the specification does not disclose a repeatable process to obtain the sequence and it is not apparent if the sequence is readily available to the public. The applicant points to the specification, Examples 1 through 6 giving ample description of how to isolate the sequence in the seeds deposited. There is

abundant description of how the process is carried out in the specification. The applicant also submits with this amendment a Statement in Support of the deposit, setting forth the parameters required for deposit of biological material pursuant to the Budapest Treaty and the criteria of 37 CFR §§1.801-1.809 and a copy of the Deposit form and receipt from the ATCC.

Claims 1, 3-4, 6-7, 9-15 and 27-34 are rejected under section 112 as not enabled. The Examiner says the specification only provides guidance for Mu mutagenesis of maize; isolation of SBMu200 male sterile plants; guidance for construction of a cDNA library and RNA expression analysis; guidance for sequencing of SBMu200 genomic sequence (SEQ ID NO: 7); sequencing of the cDNA clones, SEQ ID NO: 1 and SEQ ID NO: 2; showing the gene is expressed at particular points in microsporogenesis; isolating the promoter (SEQ ID NO: 5); and deletion analysis of the promoter. The Examiner finds this does not provide guidance for isolating a SBMu200 gene from a plant, or a nucleic acid hybridizing to SEQ ID NO: 7 under stringent conditions such that the sequence mediates fertility.

The applicant respectfully traverses the rejection. As the Examiner has pointed out, the structure of the sequence is shown, both as cDNA clones, and genomic DNA and as found in another species. Its expression pattern and analysis is set forth in Example 3, showing its expression in tassel RNA. The steps of cloning the sequence are shown, with the structure and variations shown in SEQ ID NO: 1, 3 and 7 and the amino acid encoded thereby and variations shown in SEQ ID NO: 2 and 4. The Examiner says no guidance is found in the specification for "highly stringent" hybridization conditions. However, at page 7, lines 18 through 27 the specifics of highly stringent conditions are set forth. At page 8, lines23-27, exemplary high stringency conditions are set forth including a wash in 2X SSC, 0.5% (w/v) SDS, at 65°C for 30 minutes. The specifics of highly stringent conditions are quite clear in the specification.

The Examiner also says that the specification does not show which nucleotides of the sequence can be altered to maintain activity of the encoded protein and maintain the promoter activity of the sequence, nor teaches how to assay the function of the protein encoded. The Examiner concludes this means one would now know whether a sequence that hybridizes to SEQ ID NO: 7 encodes a protein with the same function. The rejection is traversed, in that the function is one that is readily assayed; the sequence is one that, when mutated, male sterility will

result. (See specification page 23, line17-18). In fact, the assay is more readily apparent that other assays; is the plant male sterile or not when the sequence is mutated? This adds to the knowledge of what sequence is encompassed within the claim. It hybridizes under the stringent conditions set forth and retains the property that if mutated, male sterility results.

The Examiner rejects claim 15, stating it is drawn to targeted mutagenesis of the SBMu200 gene within a plant. The claim recites that expression of the nucleotide sequence is repressed by mutation of the sequence. The Examiner provides a number of calculations asserting that mutating at any one point leads to undue experimentation. The claim from which claim 15 ultimately depend, claim 12, is amended to recite that the mutation is to the nucleotide sequence of claim 3. Mutating a sequence in order to stop the expression of the sequence does not require undue experimentation. It involves procedures readily available to one skilled in the art. The identification of the essential regions of the SBMu200 promoter as described in the specification at pages 21-23, Example 5, is one example of how such mutations are routinely carried out. Deletion analysis is carried out, using site-directed mutagenesis, mutagenesis using polymerase chain reaction amongst various procedures available. (See page 21, l. 28-31, citing Directed Mutagenesis: A Practical Approach; IRL press; (1991)). Mutational analysis by linker scanner is another method well known to the art, and described in the specification, which can identify sequences essential for expression. The analysis is straightforward; is there expression of the sequence or does the promoter initiate transcription or not? It is neither necessary nor logical to make all possible single amino acid substitutions as the Examiner implies. The claim is not to every single mutation that is possible. The claim is to the sequence, those which hybridize under stringent conditions, and the method (not sequence) of claim 15 where that sequence is mutated and its expression is repressed.

Similarly, the use of antisense to inhibit expression has been used for many years, but the Examiner points to several comments by authors that one must find constructs homologous to the target gene, that the rate of transcription of antisense relative to antisense is important, as is localization of the antisense gene in the genome and length of the complementarity and special considerations when suppressing through antisense the same gene in different plant species. Accepting all this as accurate, antisense is nevertheless used frequently by those skilled in the art.

These considerations pointed out by the Examiner are those that a person skilled in the area must keep in mind. If antisense is the method to be used by the scientists skilled in this area in repressing expression of this sequence, the skilled person will keep all these parameters in mind. It does not make antisense impossible to use in repressing expression of any sequence, much less this particular sequence. Indeed, scientists have reduced or eliminated expression of a gene and affected phenotype with a wide variety of genes and phenotypes, including using antisense to induce male sterility. Such was the case as reported by Goetz et al. at "Induction of male sterility in plants by metabolic engineering of the carbohydrate supply" *PNAS,* Vol. 98, No. 11 6522-6527, May 22, 2001. There a gene encoding isoenzyme *Nin88* from tobacco was cloned and believed to be critical to male fertility. The authors introduced an antisense construct of the *Nin88* gene which resulted in blocking of early stages of pollen development and caused male sterility. Many other examples exist demonstrating that antisense regulation of expression of a gene is a process available to one skilled in the art. For example, see: Stone et al. "A breakdown of *Brassica* self-incompatibility in *ARC1* antisense transgenic plants" *Science,* Vol. 286, 1729-1731, November 26, 1999; Lally et al. "Antisense expression of a cell wall-associated protein kinase, WAK4 inhibits cell elongation and alters morphology" *Plant Cell* Vol. 13, 1317-1332, June 2001; Tabata et al. "Generation and properties of ascorbic acid-deficient transgenic tobacco cells expressing antisense RNA for L-galactono-1,4-lactone dehydrongenase" *The Plant Journal* Vol. 27(2) 139-148, 2001; Tronchet, M. "HSR203 antisense suppression in tobacco accelerates development of hypersensitive cell death" *Plant J.* Vol. 27(2), 115-27, July 2001; and Schiene et al. "Transgenic tobacco plants that express an antisense construct derived from a *Medicago sativa* cDNA encoding a Rac-related small GTP-binding protein fail to develop necrotic lesions upon elicitor infiltration" *Mol. Gen. Genet.* Vol. 263(5), 761-70 June 2000.

The Examiner continues that the specification does not show guidance for a sequence comprising the SBMu200 gene. Claim 1 is cancelled, thus making such rejection moot.

The Examiner rejects claims 1, 3-4, 607, 9-15 and 27-33 for being indefinite. Claim 1 is cancelled and thus the rejection is rendered moot. Claim 12 is amended to recite the nucleotide sequence of claim 3. Claim 29 is withdrawn.

Claim 3 is amended to delete language of a DNA molecule and now recites a nucleotide sequence comprising the sequences of those recited.

The Examiner finds indefinite use of the term "mediates" fertility in Claim 3. The claim has been amended to use instead the term "impacts" fertility, which is discussed in the specification, for example, at page 4, lines 14-23, and page 6, lines 10-29. Claim 32 is also so amended.

As proposed by the Examiner, claims 3 and 13 are amended to recite the specific wash conditions for highly stringent conditions, as discussed in the specification at page 8, lines 23-27, stating exemplary high stringency conditions are a wash in 2X SSC, 0.5% (w/v) SDS, at 65°C for 30 minutes.

Claims 6 and 9 are provided antecedent basis for recitation of a nucleotide sequence with the amendment to claim 3 reciting a nucleotide sequence.

The Examiner finds claims 12-13 indefinite in reciting "impacting." The term is used in the specification, for example, at page 4, lines 14-23, and page 6, lines 10-29, and makes clear it is consistent with the dictionary definition of impacting as "to have an impact on"; "to impinge on" and "an impinging and impinging as "to have an effect on." (www.m-w/cgo-bin/dictionary?book=Dictionary&va-impact&x=15&y=10 and (www.m-w/cgo-bin/dictionary?book=Dictionary&va-impinge&x=12&y=10; Webster's Ninth New Collegiate Dictionary , Merriam-Webster Inc., 1986). As the specification discusses, the manipulation of the sequence controls fertility; it can be used to turn male fertility or "off" by its lack of expression or back "on" when expression is restored. A sequence found to be critical to male fertility, as here, can be used to impact male fertility in a plant in such a manner. The Examiner says it is unclear how doing anything to the gene which may not be in a plant would affect fertility of the plant. Claim 13 already requires the gene be in the plant. Claim 12 is amended to add such recitation.

As proposed by the Examiner, a comma has been added in claim 13 between "4" and "the." Further, it is believed any confusion is removed by the addition of the word "or" after the comma which was inadvertently deleted in the prior amendment. Thus it is clear that the method comprises impacting any one of the sequences recited.

The amendments already discussed address the remaining issues raised by the Examiner to provide antecedent basis for recitation of nucleotide sequences in claims 14 and 15, and claim 27 now depends from the nucleotide sequence of claim 3.

Claims 28-30 and 32 should be grouped with the promoter sequence of the application and thus are not within the elected species. Applicant has withdrawn these claims.

Claim 32 is amended to remove recitation of "the promoter."

Section 102 rejection

Claim 3 is rejected under section 102(a) as anticipated by sequences appearing in GenBank, Walbot (2000, GenBank Accession Nos: AW519943 and AW424821) and Anderson et al., 2000 GenBank Accession No: BE494080. Also cited is Albertsen et al, US Patent 5,850,014 under section 102(b) as showing a nucleic acid SEQ ID NO: 1 which would hybridize under stringent conditions, the Examiner states, to the present sequence.

The applicant respectfully traverses the rejection. There is no basis to believe that these sequences would hybridize to the sequences of the invention under conditions of high stringency, and under the wash conditions set forth in the claims.

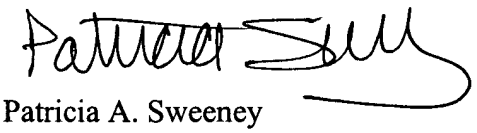
The novelty rejection based upon based homology with previously disclosed sequences in U.S. 5,850,014 which shows the MS45 gene, is not supported, since no sequences disclosed within the patent would hybridize to the applicant's claimed sequences at high stringency. Thorough comparison of the sequences disclosed in the patent with the applicants' claimed sequences shows that no imperfectly matched DNA:DNA duplexes could be formed with sufficient homology to hybridize with any sequences in the present application at the stringency hybridization condition claimed herein.

Further, as reflected in the attached affidavit of Inventor Tim Fox, the conception and reduction to practice of the invention occurred before the dates the Genbank references were made available to the public. The earliest date is February 2000, and the conception and reduction to practice of the invention occurred prior to this date. Thus, pursuant to the section 1.131 affidavit, withdrawal of the rejection on the basis of these references is respectfully requested.

The sequences are new, and no evidence exists that previously existing sequences would hybridize under the highly stringent conditions as set forth in the claims. For these reasons withdrawal of the section 102 rejection is requested. Claims 32 and 34 are found to be free of prior art and thus are in condition for allowance.

For the foregoing reasons, reconsideration and allowance of the claims is respectfully requested.

Respectfully submitted,



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